

In the Claims (clean copy as amended)

1. (Three Times Amended) An isolated and purified bacterial reverse transcriptase

Sub 2  
(RT) which synthesizes msDNA, which is essential for the synthesis of msDNA *in vivo*, and which RT comprises a sequence of amino acid residues as follows: Tyr-Xaa<sub>6</sub>-Asp-Asp (SEQ ID No:50), wherein Xaa<sub>6</sub> is alanine or cysteine and further comprising a sequence of amino acid residues as follows: Asn-Xaa<sub>1</sub>-Xaa<sub>2</sub>, wherein Xaa<sub>1</sub> is a hydrophobic residue selected from the group consisting of alanine, leucine, and phenylalanine, and Xaa<sub>2</sub> is a hydrophobic residue selected from the group consisting of leucine, valine, and isoleucine.

K2  
2. (Three Times Amended) The bacterial RT of claim 1 which contains a second sequence of amino acid residues as follows: Ser-Xaa<sub>3</sub>-Xaa<sub>4</sub>-Xaa<sub>5</sub>, wherein Xaa<sub>3</sub> is a hydrophobic residue selected from the group consisting of valine, phenylalanine, leucine, and isoleucine, Xaa<sub>4</sub> is a polar residue selected from the group consisting of threonine, asparagine, lysine, and serine, and Xaa<sub>5</sub> is a hydrophobic residue selected from the group consisting of tryptophan, phenylalanine, and alanine, as shown in SEQ ID No:51.

K3  
4. (Three Times Amended) The bacterial RT of claim 2 which contains a fourth sequence of amino acid residues as follows: Xaa<sub>7</sub>-Val-Thr-Gly, wherein Xaa<sub>7</sub> is a polar residue selected from the group consisting of arginine, glutamic acid, lysine, valine, and glutamine, as shown in SEQ ID No:45.

7. (Three Times Amended) An isolated and purified bacterial reverse transcriptase (RT) which synthesizes msDNA and which is essential for the synthesis of msDNA *in vivo*, said RT comprising a sequence of amino acid residues as follows: Tyr-Xaa<sub>6</sub>-Asp-Asp, wherein Xaa<sub>6</sub> is alanine or cysteine, as shown in SEQ ID No:50, wherein said sequence is located in subdomain 5 shown in Fig. 14 at positions 175-191 of SEQ ID No:32, at positions 175-191 of SEQ ID No:33, at positions 175-191 of SEQ ID No: 34, at positions 168-184 of SEQ ID No: 35, at positions 159-175 of SEQ ID No:36, at positions 171-187 of SEQ ID No:37, and at positions 157-173 of SEQ ID No:38, and further comprising the 61 amino acid residues as shown by black dots in Figure 14 of SEQ ID NOs:32-28, wherein h is a hydrophobic residue and p is a small polar residue.

10. (Amended) A reverse transcriptase extension *in vitro* screening test method for determining the presence or absence of msDNA in a bacterium comprising:

treating a preparation of total RNA extracted from said bacterium with a reverse transcriptase in the presence of a radiolabeled deoxynucleotide, wherein said RT, when msDNA is present in the total RNA of the bacterium, utilizes the DNA portion of the msDNA as a primer and the RNA portion of the msDNA as a template for radiolabeling the DNA portion of the msDNA, and wherein said RT comprises a sequence of amino acid residues as follows: Tyr-Xaa<sub>6</sub>-Asp-Asp (SEQ ID No:50) where Xaa<sub>6</sub> is alanine or cysteine, and a sequence of amino acid residues as follows: Asn-Xaa<sub>1</sub>-Xaa<sub>2</sub>, wherein Xaa<sub>1</sub> is a hydrophobic residue selected from the group consisting of alanine, leucine, and

phenylalanine, and Xaa<sub>2</sub> is a hydrophobic residue selected from the group consisting of leucine, valine, and isoleucine

electrophoresing the treated RNA preparation, and

determining the presence of msDNA in the bacterium by detecting a band of radiolabeled DNA, said band being indicative of the presence of msDNA in the bacterium,

wherein said bacterium is selected from the group of genera consisting of Myxococcus, Proteus, Klebsiella, Flexabacter, Cytophaga, Stigmatella, Salmonella, Nannocystis, Rhizobium, and Bradyrhizobium.

12. (Three Times Amended) The isolated and purified RT of claim 4 which RT has in the following order starting from the N- to the C-terminus:

(1) an amino acid sequence of Ser-Xaa<sub>3</sub>-Xaa<sub>4</sub>-Xaa<sub>5</sub> (SEQ ID No: 51), wherein Xaa<sub>3</sub> is a hydrophobic residue selected from the group consisting of valine, phenylalanine, leucine, and isoleucine, Xaa<sub>4</sub> is a polar residue selected from the group consisting of threonine, asparagine, lysine, and serine, and Xaa<sub>5</sub> is a hydrophobic residue selected from the group consisting of tryptophan, phenylalanine, and alanine;

(2) an amino acid sequence of Asn-Xaa<sub>1</sub>-Xaa<sub>2</sub>, where Xaa<sub>1</sub> is a hydrophobic residue selected from the group consisting of alanine, leucine, and phenylalanine, and Xaa<sub>2</sub> is a hydrophobic residue selected from the group consisting of leucine, valine, and isoleucine;

(3) an amino acid sequence Tyr-Xaa<sub>6</sub>-Asp-Asp (SEQ ID No: 50) wherein Xaa<sub>6</sub> is alanine or cysteine; and

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K6  
cont

(4) an amino acid sequence Xaa<sub>7</sub> is a polar residue selected from the group consisting

of arginine, lysine, glutamic acid, glutamine, and valine.

K7

15. (Amended) An isolated and purified reverse transcriptase which is a prokaryotic reverse transcriptase, which comprises a YXDD (tryosine-X-aspartic acid-aspartic acid) box and an amino acid sequence Asn-Xaa<sub>1</sub>-Xaa<sub>2</sub>, wherein Xaa<sub>1</sub> is a hydrophobic residue selected from the group consisting of alanine, leucine, and phenylalanine, and Xaa<sub>2</sub> is a hydrophobic residue selected from the group consisting of leucine, valine, and isoleucine.

K8

17. (Three Times Amended) The isolated and purified bacterial reverse transcriptase (RT) of claim 1 which RT has in the following order starting from N- to the C- terminus, an amino acid sequence of Asn-Xaa<sub>1</sub>-Xaa<sub>2</sub>, where Xaa<sub>1</sub> is a hydrophobic residue selected from the group consisting of alanine, leucine and phenylalanine and Xaa<sub>2</sub> is a hydrophobic residue selected from the group consisting of leucine, valine and isoleucine, an amino acid sequence of Ser-Xaa<sub>3</sub>-Xaa<sub>4</sub>-Xaa<sub>5</sub> (SEQ ID: 51), wherein Xaa<sub>3</sub> is a hydrophobic residue selected from the group consisting of valine, phenylalanine, leucine and isoleucine, Xaa<sub>4</sub> is a polar residue selected from the group consisting of threonine, asparagine, lysine and serine, and Xaa<sub>5</sub> is a hydrophobic residue selected from the group consisting of tryptophan, phenylalanine and alanine, an amino acid sequence of Tyr-Xaa<sub>6</sub>-Asp-Asp (SEQ ID No: 50), where Xaa<sub>6</sub> is alanine or cysteine, an amino acid sequence of

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cont Xaa<sub>7</sub>-Val-Thr-Gly (SEQ ID No: 52), where Xaa<sub>7</sub> is a polar residue selected from the group consisting of arginine, lysine, glutamic acid, glutamine and valine.

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Please cancel Claims 3, 9, 11, 13 and 14 without prejudice and without disclaimer of the subject matter contained therein.